

#8

PCT09

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/857,583

DATE: 06/27/2001

TIME: 15:08:50

Input Set : A:\ES.txt

Output Set: N:\CRF3\06272001\I857583.raw

3 <110> APPLICANT: Browse, John et al.
 5 <120> TITLE OF INVENTION: DESATURASES AND METHODS OF USING THEM FOR SYNTHESIS OF
 POLYUNSATURATED

6 FATTY ACIDS

8 <130> FILE REFERENCE: 4630-58963

C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/857,583

C--> 10 <141> CURRENT FILING DATE: 2001-06-05

10 <150> PRIOR APPLICATION NUMBER: US 60/111,301

11 <151> PRIOR FILING DATE: 1998-12-07

13 <150> PRIOR APPLICATION NUMBER: PCT/US99/28655

14 <151> PRIOR FILING DATE: 1999-12-06

16 <160> NUMBER OF SEQ ID NOS: 13

18 <170> SOFTWARE: PatentIn version 3.1

20 <210> SEQ ID NO: 1

21 <211> LENGTH: 1461

22 <212> TYPE: DNA

23 <213> ORGANISM: Caenorhabditis elegans

25 <400> SEQUENCE: 1

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| 26 | gaattttcaa | tcctccttgg | gtcccaccgc | tgtgatatca | aaatggtatt | acgagagcaa | 60 |
| 28 | gagcatgagc | cattcttcat | taaaattgat | ggaaaatggt | gtcaaattga | cgatgctgtc | 120 |
| 30 | ctgagatcac | atccaggtgg | tagtgcaatt | actacctata | aaaatatgga | tgccactacc | 180 |
| 32 | gtattccaca | cattccacat | tggttctaaa | gaagcgtatc | aatggctgac | agaattgaaa | 240 |
| 34 | aaagagtgcc | ctacacaaga | accagagatc | ccagatatta | aggatgaccc | aatcaaagga | 300 |
| 36 | attgatgatg | tgaacatggg | aactttcaat | atttctgaga | aacgatctgc | ccaaataaat | 360 |
| 38 | aaaagtttca | ctgatctacg | tatgcgagtt | cgtgcagaag | gacttatgga | tggatctcct | 420 |
| 40 | ttgtttctaca | ttagaaaaat | tcttgaaaca | atcttcacaa | ttctttttgc | attctacctt | 480 |
| 42 | caataccaca | catattatct | tccatcagct | attctaattg | gagttgcgtg | gcaacaattg | 540 |
| 44 | ggatgggttaa | tccatgaatt | cgcacatcat | cagttgttca | aaaacagata | ctacaatgat | 600 |
| 46 | ttggccagct | atttcgttgg | aaacttttta | caaggattct | catctggtgg | ttggaaagag | 660 |
| 48 | cagcacaatg | tgcatacgc | agccacaaat | gttggtggac | gagacggaga | tcttgattta | 720 |
| 50 | gtcccattct | atgctacagt | ggcagaacat | ctcaacaatt | attctcagga | ttcatgggtt | 780 |
| 52 | atgactctat | tcagatggca | acatgttcat | tggacattca | tgttaccatt | cctccgtctc | 840 |
| 54 | tcgtggcttc | ttcagtcaat | catttttgtt | agtcagatgc | caactcatta | ttatgactat | 900 |
| 56 | tacagaaata | ctgcgattta | tgaacagggt | ggtctctctt | tgactgaggc | ttggtcattg | 960 |
| 58 | ggtcaattgt | atttcttacc | cgattggtca | actagaataa | tgttcttctt | tgtttctcat | 1020 |
| 60 | cttggttgag | gtttcttget | ctctcatgta | gttactttca | atcattatc | agtggagaag | 1080 |
| 62 | tttgcatgga | gctogaacat | catgtcaaat | tacgcttgtc | ttcaaatcat | gaccacaaga | 1140 |
| 64 | aatatgagac | ctggaagatt | cattgactgg | ctttggggag | gtcttaacta | tcagattgag | 1200 |
| 66 | caccatcttt | tcccaacgat | gccacgacac | aacttgaaca | ctggtatgcc | acttggttaag | 1260 |
| 68 | gagtttgcag | cagcaaatgg | tttaccatac | atggtcgacg | attatttcac | aggattctgg | 1320 |
| 70 | cttgaaattg | agcaattccg | aaatattgca | aatgttgctg | ctaaattgac | taaaaagatt | 1380 |
| 72 | gcctagatta | cgattaatta | atcaatttat | tttcatgttc | tattcgtgtg | ttttaatatt | 1440 |
| 74 | ttccaaattt | ttacctattc | c | | | | 1461 |

77 <210> SEQ ID NO: 2

78 <211> LENGTH: 447

79 <212> TYPE: PRT

80 <213> ORGANISM: Caenorhabditis elegans

82 <400> SEQUENCE: 2

ENTERED

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Input Set : A:\ES.txt

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84 Met Val Leu Arg Glu Gln Glu His Glu Pro Phe Phe Ile Lys Ile Asp
85 1      5      10      15
88 Gly Lys Trp Cys Gln Ile Asp Asp Ala Val Leu Arg Ser His Pro Gly
89      20      25      30
92 Gly Ser Ala Ile Thr Thr Tyr Lys Asn Met Asp Ala Thr Thr Val Phe
93      35      40      45
96 His Thr Phe His Thr Gly Ser Lys Glu Ala Tyr Gln Trp Leu Thr Glu
97      50      55      60
100 Leu Lys Lys Glu Cys Pro Thr Gln Glu Pro Glu Ile Pro Asp Ile Lys
101 65      70      75      80
104 Asp Asp Pro Ile Lys Gly Ile Asp Asp Val Asn Met Gly Thr Phe Asn
105      85      90      95
108 Ile Ser Glu Lys Arg Ser Ala Gln Ile Asn Lys Ser Phe Thr Asp Leu
109      100      105      110
112 Arg Met Arg Val Arg Ala Glu Gly Leu Met Asp Gly Ser Pro Leu Phe
113      115      120      125
116 Tyr Ile Arg Lys Ile Leu Glu Thr Ile Phe Thr Ile Leu Phe Ala Phe
117      130      135      140
120 Tyr Leu Gln Tyr His Thr Tyr Tyr Leu Pro Ser Ala Ile Leu Met Gly
121 145      150      155      160
124 Val Ala Trp Gln Gln Leu Gly Trp Leu Ile His Glu Phe Ala His His
125      165      170      175
128 Gln Leu Phe Lys Asn Arg Tyr Tyr Asn Asp Leu Ala Ser Tyr Phe Val
129      180      185      190
132 Gly Asn Phe Leu Gln Gly Phe Ser Ser Gly Gly Trp Lys Glu Gln His
133      195      200      205
136 Asn Val His His Ala Ala Thr Asn Val Val Gly Arg Asp Gly Asp Leu
137      210      215      220
140 Asp Leu Val Pro Phe Tyr Ala Thr Val Ala Glu His Leu Asn Asn Tyr
141 225      230      235      240
144 Ser Gln Asp Ser Trp Val Met Thr Leu Phe Arg Trp Gln His Val His
145      245      250      255
148 Trp Thr Phe Met Leu Pro Phe Leu Arg Leu Ser Trp Leu Leu Gln Ser
149      260      265      270
152 Ile Ile Phe Val Ser Gln Met Pro Thr His Tyr Tyr Asp Tyr Tyr Arg
153      275      280      285
156 Asn Thr Ala Ile Tyr Glu Gln Val Gly Leu Ser Leu His Trp Ala Trp
157      290      295      300
160 Ser Leu Gly Gln Leu Tyr Phe Leu Pro Asp Trp Ser Thr Arg Ile Met
161 305      310      315      320
164 Phe Phe Leu Val Ser His Leu Val Gly Gly Phe Leu Leu Ser His Val
165      325      330      335
168 Val Thr Phe Asn His Tyr Ser Val Glu Lys Phe Ala Leu Ser Ser Asn
169      340      345      350
172 Ile Met Ser Asn Tyr Ala Cys Leu Gln Ile Met Thr Thr Arg Asn Met
173      355      360      365
176 Arg Pro Gly Arg Phe Ile Asp Trp Leu Trp Gly Gly Leu Asn Tyr Gln
177      370      375      380
180 Ile Glu His His Leu Phe Pro Thr Met Pro Arg His Asn Leu Asn Thr

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181 385          390          395          400
184 Val Met Pro Leu Val Lys Glu Phe Ala Ala Ala Asn Gly Leu Pro Tyr
185          405          410          415
188 Met Val Asp Asp Tyr Phe Thr Gly Phe Trp Leu Glu Ile Glu Gln Phe
189          420          425          430
192 Arg Asn Ile Ala Asn Val Ala Ala Lys Leu Thr Lys Lys Ile Ala
193          435          440          445
196 <210> SEQ ID NO: 3
197 <211> LENGTH: 1275
198 <212> TYPE: DNA
199 <213> ORGANISM: Euglena gracilis
201 <400> SEQUENCE: 3
202 atttttttttc gaaatgaagt caaagcgcca agcgctatcc cccttacaat tgatggaaca      60
204 aacatatgat gtggtcaatt tccaccctgg tgggtcggaa attatagaga attaccaagg      120
206 aagggatgcc actgatgcct tcattggttat gcactttcaa gaagccttcg acaagctcaa      180
208 gcgcatgccc aaaatcaatc ccagttttga gttgccaccc caggctgcag tgaatgaagc      240
210 tcaagaggat ttccggaagc tccgagaaga gttgatcgca actggcatgt ttgatgcctc      300
212 cccctctctg tactcataca aaatcagcac cacactgggc cttggagtgc tgggttattt      360
214 cctgatgggt cagtatcaga tgtatttcat tggggcagtg ttgcttgga tgcactatca      420
216 acagatgggc tggctttctc atgacatttg ccaccaccag actttcaaga accggaactg      480
218 gaacaacctc gtgggactgg tatttgga tggctcgcaa ggtttttccg tgacatgttg      540
220 gaaggacaga cacaatgcac atcattcggc aaccaatgtt caagggcacg accctgatat      600
222 tgacaacctc cccccccttag cctggctctga ggatgacgtc acacgggcgt caccgatttc      660
224 ccgcaagctc attcagttcc agcagtacta tttcttggtc atctgtatct tgttgcggtt      720
226 catttggtgt ttccagtgcg tgttgaccgt gcgcagtttg aaggacagag ataaccaatt      780
228 ctatcgtctc cagtataaga aggaggccat tggcctcgcc ctgcactgga cettgaaggc      840
230 cctgttccac ttattcttta tgcccagcat cctcacatcg ctggttggtgt ttttcgtttc      900
232 ggagctggtt ggcggtctcg gcattgcgat cgtggtgttc atgaaccact acccactgga      960
234 gaagatcggg gaccagctct gggatggcca tggattctcg gttggccaga tccatgagac      1020
236 catgaacatt cggcgaggga ttatcacaga ttggttttcc ggaggcttga attaccagat      1080
238 tgagcaccat ttgtggccga cctcctctcg ccacaacctg acagcggtta gctaccaggt      1140
240 ggaacagctg tgccagaagc acaacctgcc gtatcggaac ccgctgcccc atgaagggtt      1200
242 ggtcatcctg ctgcgctatc tggcgggtgt cgcccgatg gcggagaagc aaccgcggg      1260
244 gaaggctcta taagg      1275
247 <210> SEQ ID NO: 4
248 <211> LENGTH: 422
249 <212> TYPE: PRT
250 <213> ORGANISM: Euglena gracilis
252 <400> SEQUENCE: 4
254 Met Lys Ser Lys Arg Gln Ala Leu Ser Pro Leu Gln Leu Met Glu Gln
255 1          5          10          15
258 Thr Tyr Asp Val Ser Ala Trp Val Asn Phe His Pro Gly Gly Ala Glu
259          20          25          30
262 Ile Ile Glu Asn Tyr Gln Gly Arg Asp Ala Thr Asp Ala Phe Met Val
263          35          40          45
266 Met His Phe Gln Glu Ala Phe Asp Lys Leu Lys Arg Met Pro Lys Ile
267          50          55          60
270 Asn Pro Ser Phe Glu Leu Pro Pro Gln Ala Ala Val Asn Glu Ala Gln
271 65          70          75          80

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274 Glu Asp Phe Arg Lys Leu Arg Glu Glu Leu Ile Ala Thr Gly Met Phe
275      85      90      95
278 Asp Ala Ser Pro Leu Trp Tyr Ser Tyr Lys Ile Ser Thr Thr Leu Gly
279      100     105     110
282 Leu Gly Val Leu Gly Tyr Phe Leu Met Val Gln Tyr Gln Met Tyr Phe
283      115     120     125
286 Ile Gly Ala Val Leu Leu Gly Met His Tyr Gln Gln Met Gly Trp Leu
287      130     135     140
290 Ser His Asp Ile Cys His His Gln Thr Phe Lys Asn Arg Asn Trp Asn
291 145      150     155     160
294 Asn Leu Val Gly Leu Val Phe Gly Asn Gly Leu Gln Gly Phe Ser Val
295      165     170     175
298 Thr Cys Trp Lys Asp Arg His Asn Ala His His Ser Ala Thr Asn Val
299      180     185     190
302 Gln Gly His Asp Pro Asp Ile Asp Asn Leu Pro Pro Leu Ala Trp Ser
303      195     200     205
306 Glu Asp Asp Val Thr Arg Ala Ser Pro Ile Ser Arg Lys Leu Ile Gln
307      210     215     220
310 Phe Gln Gln Tyr Tyr Phe Leu Val Ile Cys Ile Leu Leu Arg Phe Ile
311 225      230     235     240
314 Trp Cys Phe Gln Cys Val Leu Thr Val Arg Ser Leu Lys Asp Arg Asp
315      245     250     255
318 Asn Gln Phe Tyr Arg Ser Gln Tyr Lys Lys Glu Ala Ile Gly Leu Ala
319      260     265     270
322 Leu His Trp Thr Leu Lys Ala Leu Phe His Leu Phe Phe Met Pro Ser
323      275     280     285
326 Ile Leu Thr Ser Leu Leu Val Phe Phe Val Ser Glu Leu Val Gly Gly
327      290     295     300
330 Phe Gly Ile Ala Ile Val Val Phe Met Asn His Tyr Pro Leu Glu Lys
331 305      310     315     320
334 Ile Gly Asp Pro Val Trp Asp Gly His Gly Phe Ser Val Gly Gln Ile
335      325     330     335
338 His Glu Thr Met Asn Ile Arg Arg Gly Ile Ile Thr Asp Trp Phe Phe
339      340     345     350
342 Gly Gly Leu Asn Tyr Gln Ile Glu His His Leu Trp Pro Thr Leu Pro
343      355     360     365
346 Arg His Asn Leu Thr Ala Val Ser Tyr Gln Val Glu Gln Leu Cys Gln
347      370     375     380
350 Lys His Asn Leu Pro Tyr Arg Asn Pro Leu Pro His Glu Gly Leu Val
351 385      390     395     400
354 Ile Leu Leu Arg Tyr Leu Ala Val Phe Ala Arg Met Ala Glu Lys Gln
355      405     410     415
358 Pro Ala Gly Lys Ala Leu
359      420
362 <210> SEQ ID NO: 5
363 <211> LENGTH: 27
364 <212> TYPE: DNA
365 <213> ORGANISM: artificial sequence
367 <220> FEATURE:

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```

368 <223> OTHER INFORMATION: PCR Primer
370 <220> FEATURE:
371 <221> NAME/KEY: misc_feature
372 <222> LOCATION: (12)..(12)
373 <223> OTHER INFORMATION: n = a, t, g, or c
376 <400> SEQUENCE: 5
W--> 377 ggctggctga cncaygartt ytgycay 27
380 <210> SEQ ID NO: 6
381 <211> LENGTH: 30
382 <212> TYPE: DNA
383 <213> ORGANISM: artificial sequence
385 <220> FEATURE:
386 <223> OTHER INFORMATION: PCR Primer
388 <220> FEATURE:
389 <221> NAME/KEY: misc_feature
390 <222> LOCATION: (13)..(13)
391 <223> OTHER INFORMATION: n = a, t, g, or c
394 <400> SEQUENCE: 6
W--> 395 catcggttggga aanaarrtgrt gytcdatytg 30
398 <210> SEQ ID NO: 7
399 <211> LENGTH: 41
400 <212> TYPE: DNA
401 <213> ORGANISM: artificial sequence
403 <220> FEATURE:
404 <223> OTHER INFORMATION: PCR Primer
406 <400> SEQUENCE: 7
407 cccgggaagc ttctcgagga attttcaatc ctccttggt c 41
410 <210> SEQ ID NO: 8
411 <211> LENGTH: 34
412 <212> TYPE: DNA
413 <213> ORGANISM: artificial sequence
415 <220> FEATURE:
416 <223> OTHER INFORMATION: PCR Primer
418 <400> SEQUENCE: 8
419 cccgggtgga tccggaacat atcacacgaa acag 34
422 <210> SEQ ID NO: 9
423 <211> LENGTH: 6
424 <212> TYPE: RNA
425 <213> ORGANISM: artificial sequence
427 <220> FEATURE:
428 <223> OTHER INFORMATION: Consensus sequence
430 <220> FEATURE:
431 <221> NAME/KEY: polyA_signal
432 <222> LOCATION: (1)..(6)
433 <223> OTHER INFORMATION:
436 <400> SEQUENCE: 9
437 aauaaa 6
440 <210> SEQ ID NO: 10
441 <211> LENGTH: 20

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Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

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Input Set : A:\ES.txt

Output Set: N:\CRF3\06272001\I857583.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:377 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:395 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:487 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:508 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13